

BASE COUNT 15 a 22 c 25 g 15 t
 ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 77;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcggggag 12
 |||||||||
 DB 21 GCCTCTGGGAG 32

RESULT 2
 LOCUS AA648867 97 bp mRNA linear EST 29-OCT-1997
 DEFINITION ns37908.s1 NCI-CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1185854 3',
 similar to TR:G984114 G984114 RIBOSOME RECEPTOR. ; mRNA sequence.
 ACCESSION AA648867
 VERSION AA648867
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 97)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 unknown library type
 Trace considered overall poor quality
 Seq primer: 40m13 fwd. ET from Amerisham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..97
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1185854"
 /clone_lib="NCI-CGAP_GCB1"
 /issue_type="germlinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTACCAATCGAGTGGAGCGCGCTCATTTTCTTTTCTTTT-3',
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 21 a 29 c 32 g 15 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 97;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcggggag 12
 |||||||||
 DB 86 GCCTCTGGGAG 75

RESULT 3
 LOCUS AM579821 117 bp mRNA linear EST 16-MAR-2000

DEFINITION RC4-HT0278-080100-012-g04 HT0278 Homo sapiens CDNA, mRNA sequence.
 AM579821
 VERSION AM579821.1 GI:7254870
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 117)
 HCGP http://www.ludwig.org.br/ORESTES.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL.
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC4&t2=RC4-HT0278-
 080100-012-g04&t3=2000-01-08&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 117.
 Location/Qualifiers
 1..117
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0278"
 /dev_strage="Adult"
 /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 23 a 38 c 24 g 32 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcggggag 12
 |||||||||
 DB 20 GCCTCTGGGAG 9

RESULT 4
 LOCUS AW769584 117 bp mRNA linear EST 04-MAY-2000
 DEFINITION h167g04.x1 NCI-CGAP_Kid3 Homo sapiens CDNA clone IMAGE:3006294 3',
 mRNA sequence.
 ACCESSION AW769584
 VERSION AW769584.1 GI:7701616
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 117)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@imga.llnl.gov
 Seq primer: -40UP from g1bco
 High quality sequence stop: 107.
 Location/Qualifiers

FEATURES

1. 117
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:3006294"
 /clone_lib="NCI-CGAP_Kid13"
 /tissue_type="2 pooled Wilms' tumors, one primary and one metastatic to brain"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dt. Library constructed by Life Technologies."
 BASE COUNT 42 a 24 c 33 g 18 t

BASE COUNT

Query Match 100.0%; Score 12; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctctggggag 12
 |||||||
 Db 105 gccctctggggag 116

RESULT 5
 AI602435 121 bp mRNA linear EST 21-APR-1999
 LOCUS AI602435/c
 DEFINITION UI-R-AGO-wz-g-05-0-UI-s1 UI-R-AGO Rattus norvegicus cDNA clone
 UI-R-AGO-wz-g-05-0-UI 3', mRNA sequence.
 ACCESSION AI602435
 VERSION AI602435.1 GI:4611596
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 121)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dt track served to verify it as a clone from the non-normalized ventricle at 13 dpc library cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Seg primer: M13 Forward.

FEATURES

Location/Qualifiers
 1. 121
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"

/db_xref="taxon:10116"
 /clone="UI-R-AGO-wz-g-05-0-UI"
 /clone_lib="UI-R-AGO"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AGO library is a non-normalized library constructed from 13 dpc rat ventricle. The tag is a string of 6 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of Iowa."
 BASE COUNT 25 a 26 c 36 g 34 t

BASE COUNT

Query Match 100.0%; Score 12; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctctggggag 12
 |||||||
 Db 51 gccctctggggag 40

RESULT 6
 BE682645 124 bp mRNA linear EST 25-APR-2001
 LOCUS BE682645
 DEFINITION 180821 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE682645
 VERSION BE682645.1 GI:10068717
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 124)
 AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitto-McKown,C.G., Perle,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@ma1.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -m1nscore 18 and -m1m1nch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACAT
 BACKWARD: GTTTCACAGTCAGCAGC
 Plate: 75 row: A column: 18
 Seg primer: ATTAGTACACTATAG.

FEATURES

Location/Qualifiers
 1. 124
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 4BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 20 and day 40 embryos."

BASE COUNT 24 a 51 c 33 g 16 t
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
Db 21 GCCTCTGGGAG 32

RESULT 7
AI712861 125 bp mRNA linear EST 08-JUN-1999
LOCUS AI712861

DEFINITION UI-R-AG1-aaf-d-03-0-UI.s2 UI-R-AG1 Rattus norvegicus cDNA clone
AI712861
VERSION UI-R-AG1-aaf-d-03-0-UI 3', mRNA sequence.
KEYWORDS AI712861.1 GI:5016661
SOURCE EST.

ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 125)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

AUTHORS Normalization and subtraction: two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT

Program for Rat Gene Discovery and Mapping
Contact: Soares, MB
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: mscoares@iuii.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward

POLYA=yes
Location/Qualifiers

FEATURES
source

1. 125
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AG1-aaf-d-03-0-UI"
/clone_1lb="UI-R-AG1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AG1
library is a normalized library constructed from 13 dpc
rat ventricle. The tag is a string of 6 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AG1
TAG_TISSUE=ventricle at 13 dpc
TAG_SEQ=CAGCGA"

BASE COUNT 27 a 27 c 36 g 35 t
ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
Db 52 GCCTCTGGGAG 41

RESULT 8
BE988071 128 bp mRNA linear EST 05-OCT-2000
LOCUS BE988071

DEFINITION UI-M-CG0P-bho-b-02-0-UI.s1 NIH_BMAP_Ret4.S2 Mus musculus cDNA clone
UI-M-CG0P-bho-b-02-0-UI 3', mRNA sequence.
ACCESSION BE988071
VERSION BE988071.1 GI:10664063
KEYWORDS EST.

SOURCE house mouse.
Mus musculus
house mouse.

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 128)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

REFERENCE Normalization and subtraction: two approaches to facilitate gene
TITLE discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=No.

FEATURES
source

Location/Qualifiers
1. 128
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0P-bho-b-02-0-UI"
/clone_1lb="NIH_BMAP_Ret4.S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4.S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"

BASE COUNT 21 a 31 c 35 g 41 t
ORIGIN

Query Match 100.0%; Score 12; DB 10; Length 128;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
Db 78 GCCTCTGGGAG 89

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES

source

1.133
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:7640485"
/db_xref="taxon:9606"
/clone="RPCI-11-366N14"
/clone_1b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI;
RPC11 Human Male BAC library"

BASE COUNT
31 a 43 c 28 g 31 t

Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 136;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.0%; Score 12; DB 12; Length 133;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 136;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
BF836463 136 bp mRNA linear EST 13-JAN-2001
LOCUS RC3-HT0974-171100-012-c02 HT0974 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF836463
ACCESSION BF836463.1 GI:12188356
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RESULT 13
AA955315/c 138 bp mRNA linear EST 04-JUL-1999
LOCUS UI-R-AI-ew-d-02-0-UI.s1 UI-R-AI Rattus norvegicus cDNA clone
DEFINITION AA955315
ACCESSION AA955315.1 GI:4237674
VERSION EST.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

REFERENCE
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On May 7, 1998 this sequence version replaced gi:3118889.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.iowa.edu

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
adult Heart library. cDNA library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics This clone is also available through the I.M.A.G.E.
Consortium at LNL (info@image.lnl.gov). IMAGE ID=1779112 The
following repetitive elements were found in this cDNA sequence:
95-129, >(GGGA)n#Simple_repeat
Seq primer: M13 Forward
POLYA-No.

FEATURES

source

1.136
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="HT0974"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; site_1: SmaI;
site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application

1.138
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AI-ew-d-02-0-UI"
/clone_1b="UI-R-AI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AI
library is a subtracted library derived from the UI-R-A0
library. The UI-R-A0 library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dr track which allows identification of the library
of origin of a clone within the mixture. The subtracted

library (UT-R-A1) was constructed as follows: PCR amplified cDNA inserts from a pool of approximately 3,840 UT-R-A0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UT-R-A0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UT-R-A1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 32 a 28 c 44 g 34 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctggggag 12
|||||

DB 51 gccctggggag 40

RESULT 14
BE151130/c 139 bp mRNA linear EST 21-JUN-2000
LOCUS BE151130
DEFINITION RC4-HT0277-160200-013-h05 HT0277 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE151130
VERSION BE151130.1 GI:8613851
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunsfeld, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC4-HT0277-160200-013-h05&t3=2000-02-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
Location/Qualifiers
1. 139
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0277"
/dev_stage="Adult"
/note="Organ: head, neck; Vector: puc18; Site: 1; Smal: Site: 2; Smal: A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of

FEATURES

tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 30 a 45 c 25 g 39 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctggggag 12
|||||

DB 43 gccctggggag 32

RESULT 15
AA980863 146 bp mRNA linear EST 27-MAY-1998
LOCUS AA980863
DEFINITION u246e10.t1 Soares_mammary_gland_NBMKG Mus musculus clone
IMAGE:1349802 5', mRNA sequence.
ACCESSION AA980863
VERSION AA980863.1 GI:3159399
KEYWORDS EST.
SOURCE mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@waterston.wustl.edu
This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:698594
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 111.
Location/Qualifiers
1. 146
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="1349802"
/clone_lib="Soares_mammary_gland_NBMKG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1; Not I; Site: 2; Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGTGGAGCGCCGCCGAGTGTGTTTTTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

FEATURES

SOURCE

BASE COUNT 32 a 29 c 52 g 33 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctggggag 12
|||||
Db 29 GCCTCTGGGAG 40

Search completed: May 10, 2002, 16:46:03
Job time: 8833 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 1906.21 Seconds
(without alignments)
131.737 Million cell updates/sec

Title: US-09-761-116-1
Sequence: 1 ggcctcggggag 12
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sls: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_cm: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sls: *
28: em_un: *
29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
|------------|-------|-------------|--------|-------|-------------|

| | | | | | | |
|----|----|-------|-----|----|------------|---------------------|
| 1 | 12 | 100.0 | 12 | 6 | AR137925 | AR137925 Sequence |
| 2 | 12 | 100.0 | 28 | 6 | AR137965 | AR137965 Sequence |
| 3 | 12 | 100.0 | 28 | 6 | AR137970 | AR137970 Sequence |
| 4 | 12 | 100.0 | 28 | 6 | AR137971 | AR137971 Sequence |
| 5 | 12 | 100.0 | 28 | 6 | AR137972 | AR137972 Sequence |
| 6 | 12 | 100.0 | 130 | 9 | HSU39347 | U93347 Human MHC C |
| 7 | 12 | 100.0 | 200 | 6 | AR137927 | AR137927 Sequence |
| 8 | 12 | 100.0 | 208 | 11 | G04524 | G04524 human STS W |
| 9 | 12 | 100.0 | 234 | 6 | AX244726 | AX244726 Sequence |
| 10 | 12 | 100.0 | 266 | 11 | G65279 | G65279 FBNI-64new |
| 11 | 12 | 100.0 | 278 | 9 | HSN1243D | X87489 H. sapiens f |
| 12 | 12 | 100.0 | 287 | 9 | HUMCWO5 | D64153 Human DNA f |
| 13 | 12 | 100.0 | 292 | 11 | G09804 | G09804 human STS C |
| 14 | 12 | 100.0 | 321 | 11 | HUMUT7961A | L30159 Human STS U |
| 15 | 12 | 100.0 | 330 | 11 | G71854 | G71854 A09122834FM |
| 16 | 12 | 100.0 | 343 | 11 | G71018 | G71018 A09122834FB |
| 17 | 12 | 100.0 | 370 | 9 | AF366903 | AF366903 Homo sapi |
| 18 | 12 | 100.0 | 381 | 6 | AX072790 | AX072790 Sequence |
| 19 | 12 | 100.0 | 384 | 10 | MMEB2AK1 | X04437 Mouse class |
| 20 | 12 | 100.0 | 393 | 10 | AF028605 | AF028605 Rattus no |
| 21 | 12 | 100.0 | 403 | 4 | AB016736 | AB016736 Sus scrof |
| 22 | 12 | 100.0 | 403 | 4 | AB016737 | AB016737 Sus scrof |
| 23 | 12 | 100.0 | 403 | 4 | AB016738 | AB016738 Sus scrof |
| 24 | 12 | 100.0 | 403 | 4 | AB016739 | AB016739 Sus scrof |
| 25 | 12 | 100.0 | 403 | 4 | AB016740 | AB016740 Sus scrof |
| 26 | 12 | 100.0 | 403 | 4 | AB016741 | AB016741 Sus scrof |
| 27 | 12 | 100.0 | 403 | 4 | AB016742 | AB016742 Sus scrof |
| 28 | 12 | 100.0 | 403 | 4 | AB016743 | AB016743 Sus scrof |
| 29 | 12 | 100.0 | 403 | 4 | AB016744 | AB016744 Sus scrof |
| 30 | 12 | 100.0 | 403 | 4 | AB016745 | AB016745 Sus scrof |
| 31 | 12 | 100.0 | 417 | 10 | AF028603 | AF028603 Rattus no |
| 32 | 12 | 100.0 | 427 | 11 | G55693 | AF028604 Rattus no |
| 33 | 12 | 100.0 | 432 | 10 | AF028604 | M21106 Mouse Induc |
| 34 | 12 | 100.0 | 437 | 10 | MUSMX103 | AB016251 Oryctolag |
| 35 | 12 | 100.0 | 439 | 4 | AB016251 | L27630 Canis faml |
| 36 | 12 | 100.0 | 534 | 4 | DOGP53A | AX312180 Sequence |
| 37 | 12 | 100.0 | 545 | 6 | AX312180 | AF300861 Peromyscu |
| 38 | 12 | 100.0 | 591 | 10 | AF300861 | AF300862 Peromyscu |
| 39 | 12 | 100.0 | 594 | 10 | AF300862 | AJ336032 Homo sapi |
| 40 | 12 | 100.0 | 596 | 9 | HSB323688 | AJ336032 Homo sapi |
| 41 | 12 | 100.0 | 599 | 9 | HSB326032 | AJ336032 Homo sapi |
| 42 | 12 | 100.0 | 599 | 9 | HSB342624 | AJ338863 Homo sapi |
| 43 | 12 | 100.0 | 606 | 9 | HSB338863 | AJ338863 Homo sapi |
| 44 | 12 | 100.0 | 612 | 9 | HSB335324 | AJ335324 Homo sapi |
| 45 | 12 | 100.0 | 612 | 9 | HSB342448 | AJ342448 Homo sapi |

ALIGNMENTS

| | | | | | | |
|------------|--|------------------------------------|-------|-----|--------|-----------------|
| RESULT 1 | AR137925 | Sequence 1 | 12 bp | DNA | linear | PAT 16-JUN-2001 |
| LOCUS | AR137925 | Sequence 1 from patent US 6197580. | | | | |
| DEFINITION | AR137925 | | | | | |
| ACCESSION | AR137925.1 | GI:14479434 | | | | |
| VERSION | | | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Unknown. | | | | | |
| ORGANISM | Unclassified. | | | | | |
| REFERENCE | 1 (bases 1 to 12) | | | | | |
| AUTHORS | Susulic,V.S. and Duzic,E. | | | | | |
| TITLE | Transcriptional regulation of the human .beta.3-adrenergic receptor gene | | | | | |
| JOURNAL | Patent: US 6197580-A 1 06-MAR-2001; | | | | | |
| FEATURES | Location/Qualifiers | | | | | |
| SOURCE | 1..12 | | | | | |
| BASE COUNT | 1 a 3 c 6 g 2 t | | | | | |
| ORIGIN | 1 a 3 c 6 g 2 t | | | | | |

Query Match 100.0%; Score 12; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 1 GCCTCTGGGAG 12

RESULT 2
ARI37965 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37965
DEFINITION Sequence 41 from patent US 6197580.
ACCESSION ARI37965
VERSION ARI37965.1 GI:14479474

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 41 06-MAR-2001;
FEATURES Location/Qualifiers

source 1..28

BASE COUNT 4 a 10 c 8 g 6 t
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 3
ARI37970 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37970
DEFINITION Sequence 46 from patent US 6197580.
ACCESSION ARI37970
VERSION ARI37970.1 GI:14479479

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 46 06-MAR-2001;
FEATURES Location/Qualifiers

source 1..28

BASE COUNT 3 a 10 c 8 g 7 t
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 4
ARI37971 28 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 47 from patent US 6197580.

ACCESSION ARI37971

VERSION ARI37971.1 GI:14479480

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 47 06-MAR-2001;
FEATURES Location/Qualifiers

source 1..28

BASE COUNT 6 a 9 c 9 g 4 t
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 5
ARI37972 28 bp DNA linear PAT 16-JUN-2001

LOCUS ARI37972
DEFINITION Sequence 48 from patent US 6197580.
ACCESSION ARI37972
VERSION ARI37972.1 GI:14479481

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)

AUTHORS Susulic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 48 06-MAR-2001;
FEATURES Location/Qualifiers

source 1..28

BASE COUNT 5 a 7 c 11 g 5 t
ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
|||||
Db 6 GCCTCTGGGAG 17

RESULT 6
HSU39347 130 bp DNA linear PRI 21-MAR-1997

LOCUS HSU39347
DEFINITION Human MHC class I antigen HLA-C gene (HLA-Cw*0401 allele), Intron

ACCESSION U39347
VERSION U39347.1 GI:1654171

KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 130)
AUTHORS Cereb.N., Kong,Y., Lee,S., Maye,P. and Yang,S.Y.

TITLE Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans and Intron 2 in nonhuman primates

JOURNAL Tissue Antigens 47 (6), 498-511 (1996)

MEDLINE 96408732

REFERENCE 2 (bases 1 to 130)

AUTHORS Yang, S.Y. and Cereb.N.

TITLE Direct Submission

JOURNAL Submitted (24-OCT-1995) Soo Yang, Immunology Program, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, Box 41, New York, NY 10021, USA

FEATURES Location/Qualifiers

source 1..130
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/cell_line="WT100BIS B cell line"
1..130
/gene="HLA-C"
1..130
/note="HLA-C*0401 allele"
/number=1

BASE COUNT 19 a 36 c 63 g 12 t

ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

DB 27 gccctcggggag 38

RESULT 7

LOCUS ARI37927 200 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 3 from patent US 6197580.

ACCESSION ARI37927

VERSION ARI37927.1 GI:14479436.

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 200)
Susulic,V.S. and Duzic,E.
Transcriptional regulation of the human .beta.3-adrenergic receptor gene

JOURNAL Patent: US 6197580-A 3 06-MAR-2001;

FEATURES Location/Qualifiers

source 1..200
/organism="unknown"

BASE COUNT 25 a 70 c 37 g 68 t

ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

DB 61 gccctcggggag 72

RESULT 8

LOCUS G04524 208 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-4034, sequence tagged site.

ACCESSION G04524

VERSION G04524.1 GI:721482

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Human Random genome wide STS created from sheared whole human DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 208)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Whitehead Institute/MIT Center for Genome Research; Random Genome wide STS

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 208)

AUTHORS Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped STS

JOURNAL Unpublished

COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TATGGCAGCTTGAGAGGG
Primer B: CCCCAAGAGAGCCATCT
STS size: 155

PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3.

FEATURES Location/Qualifiers

source 1..208
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="709.B.4; 802.B.4; 805.F.5; 851.E.2; 964.F.8;
921.A.10; (720,724)_A_(10,12); 304.8 CR from top of Chr15
linkage group"

STS 51..205

primer_bind 51..70

BASE COUNT complement(188..205)
51 a 43 c 69 g 45 t

ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcggggag 12
|||||

DB 14 gccctcggggag 25

RESULT 9

LOCUS AX244726 234 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 55 from Patent WO0166750.

ACCESSION AX244726 GI:15859605
 VERSION AX244726.1
 KEYWORDS
 SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 234)
 AUTHORS Vogel, G. and Wood, L.S.
 TITLE G protein-coupled receptors
 JOURNAL Patent: WO 0166750-A 55 13-SEP-2001;
 PHARMACIA & UPJOHN COMPANY (US)
 FEATURES
 source
 Location/Qualifiers
 1..234
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 56 a 64 c 65 g 49 t
 ORIGIN

Query Match 100.0%; Score 12; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. NO. 4.2e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 100 GCCTCTGGGAG 111

RESULT 10
 G65279 266 bp DNA linear STS 14-JUL-2000
 LOCUS FBNI-64new Random genomic STS Homo sapiens STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION G65279
 VERSION G65279.1 GI:9211115
 KEYWORDS STS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Oefner, P.J.
 TITLE Human random genomic STS survey, unpublished data
 JOURNAL Unpublished
 COMMENT
 Contact: Peter Oefner
 Stanford Genome Center
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 6508121926
 Fax: 6508121975
 Email: Oefner@genome.stanford.edu
 Primer A: CCTACCTTCTCTCCCACTTAA
 Primer B: ACAGAGACATCAGGAGAACTAAC
 STS size: 266
 PCR Profile:
 Initial denaturing step of 95 degrees C for 10 min to activate
 AmpliTaq Gold (1
 min for AmpliTaq);
 14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
 min at 63
 degrees C to
 56 degrees C using decrements of 0.5 degrees C, extension at 72
 degrees C for 1
 min;
 20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
 degrees C for 1
 min.
 Protocol:
 Template: 50 ng
 Primer: each 0.2 uM
 Taq Polymerase: 0.02 units/ul

Total Vol: 50 ul

Buffer: 2.5 mM
 MgCl2: 50 mM
 KCl: 10 mM
 Tris-HCl: 8.3
 pH: 8.3
 DMSO: 0 %

FEATURES
 source
 Location/Qualifiers
 1..266
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /sex="Male and Female"
 /clone_lib="Random genomic STS"
 1..266
 primer_bind 1..23
 primer_bind complement(242..266)
 BASE COUNT 69 a 68 c 65 g 64 t
 ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 266;
 Best Local Similarity 100.0%; Pred. NO. 4.1e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 145 GCCTCTGGGAG 134

RESULT 11
 HSNL1243D 278 bp DNA linear PRI 01-JUL-1996
 LOCUS HSNL1243D
 DEFINITION H.sapiens genomic DNA (chromosome 3; clone N1243D).
 ACCESSION X87489
 VERSION X87489.1 GI:1418839
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 278)
 AUTHORS Zabarovsky, E.R.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 278)
 AUTHORS Zabarovsky, E.R.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAY-1995) Zabarovsky E.R., Microbiology and
 Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm,
 S-171 77, SWEDEN
 FEATURES
 source
 Location/Qualifiers
 1..278
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3 (human)"
 /cell_line="mouse/human microcell hybrid line MHC 903.1"
 /clone_lib="NotI linking library"
 /clone="N1243D"
 /note="genomic DNA surrounding NotI sites"
 BASE COUNT 44 a 95 c 77 g 62 t
 ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 278;
 Best Local Similarity 100.0%; Pred. NO. 4.1e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctctggggag 12
 |||||||||
 Db 240 GCCTCTGGGAG 251

RESULT 12

HUMC05/c
LOCUS HUMC05 287 bp DNA linear PRI 14-APR-2000
DEFINITION Human DNA for HLA-Cw*0702, partial cds.
ACCESSION D64153
VERSION D64153.1 GI:1339908
KEYWORDS HLA-Cw*0702; MHC class I.
SOURCE Homo sapiens (Isolate:TM) peripheral blood lymphocyte DNA, clone:U-1.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (sites)
AUTHORS Wang, H., Tokunaga, K., Ishikawa, Y., Asahina, A., Kuwata, S., Akaza, T., Tadokoro, K., Shibata, Y., Takiguchi, M. and Uji, T.
TITLE Identification and DNA typing of two Cw7 alleles (Cw*0702 and Cw*0704) in Japanese, with the corrected sequence of Cw*0702
JOURNAL Hum. Immunol. 45 (1), 52-58 (1996)
MEDLINE 96232973
REFERENCE 2 (bases 1 to 287)
AUTHORS Wang, H.
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 287)
AUTHORS Wang, H.
TITLE Direct Submission
SUBMITTED (16-SEP-1995) Huiru Wang, Japanese Red Cross Central Blood Center, Department of Research; 4-1-31 Hiroo, Shibuya-ku, Tokyo 150, Japan (Tel:03-3465-6009, Fax:03-3406-7892)
FEATURES
source
1..287
/organism="Homo sapiens"
/isolate="TM"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/clone="U-1"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
1..157
/number=1
5'UTR
1..84
85..>157
/codon_start=1
/product="HLA-Cw*0702"
/protein_id="BAI1022.1"
/db_xref="GI:1561555"
/translation="MKVMAFRLLILSLALLETWA"
158..287
/number=1
BASE COUNT 45 a 101 c 103 g 38 t
ORIGIN
Intron
Query Match 100.0%; Score 12; DB 9; Length 287;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gacctctggagg 12
|||||
Db 80 GCCTCTGGGAG 69.
RESULT 13
LOCUS G09804 292 bp DNA linear STS 15-AUG-1995
DEFINITION human STS CHLC.GCT13C07.P16417 clone GCT13C07, sequence tagged site.
ACCESSION G09804
VERSION G09804.1 GI:941653
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE human vector-pUCP1 host-E.coli dutung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 292)
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buettow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished
COMMENT Synonyms: GCT13C07, CHLC.GCT13C07.T16344
Contact: Dr. Jeffrey C. Murray
ncfi
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@iowa.edu
Primer A: TTCGACCTTACCATGTTGATCC
Primer B: GTTCACCTGACACAGTTCCC
STS size: 122
PCR Profile:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 uL
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3
1..292
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
62..183
primer_bind
62..86
complement(164..183)
BASE COUNT 86 a 60 c 58 g 86 t 2 others
ORIGIN
Query Match 100.0%; Score 12; DB 11; Length 292;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gacctctggagg 12
|||||
Db 219 GCCTCTGGGAG 230
RESULT 14
LOCUS HUMUT7961A/c 321 bp DNA linear STS 29-DEC-1994
DEFINITION Human STS UT7961, 5' primer bind, sequence tagged site.
ACCESSION L30159
VERSION L30159.1 GI:605335
KEYWORDS STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Wells, R., Lawrence, E., Moore, P., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsnier, T., Tingey, A., Lalouel, J.-M. and White, R.
TITLE Genetic and physical mapping of simple sequence repeat containing

JOURNAL
COMMENT

Sequence tagged sites from the human genome
Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics

2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112

e-mail: stg@corona.med.utah.edu

Primer A: TTGGACTCCCGAGGCGT
Primer B: TTGGCTGGCGGTGAGTTT

End to Label: Primer A
PCR Profile:

Initial Denaturation: 94C 300sec
Cycles Denaturation: 94C 30 sec. Extension 5 94

C 10 sec. 34 C 10 sec. 72 C 20 sec. 30
56 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM

gel: Acrylamide 7%, Formamide 32%, Urea 34%

Alleles: 1.
Location/Qualifiers

1.321
/organism="Homo sapiens"

primer_bind
/db_xref="taxon:9606"

BASE COUNT 64 a 102 c 97 g 53 t 5 others
ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 321;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctgaggag 12
|||||
DB 213 GCCTCTGGGAG 202

RESULT 15

G71854 330 bp DNA linear STS 08-JUN-2001
LOCUS A09122834FW017 maize leaf DNA Zea mays STS genomic, sequence tagged

DEFINITION site.

ACCESSION G71854 GI:1433539

VERSION G71854.1

KEYWORDS STS.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 330)
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
3' UTR sequences of maize genes
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Schnable, P.S.
Schnable Laboratory
Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA

Tel: 515-294-0975
Fax: 515-294-2299

Email: schnable@iastate.edu

Primer A: CCTATCTATGGCTTCACG
Primer B: GGAGAGGCTGATCATCG

PCR Profile:

Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds

PCR cycles: 31

Thermal cycler: Perkin Elmer TC

Protocol:

Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM

Tag Polymerase: 0.05 units/ul
Total vol: 20 ul

Buffer:

MgCl2: 2 mM
KCl: 50 mM
Tris-HCl: 20 mM

pH: 8.4

FEATURES
source

1.330
/organism="Zea mays"

/strain="DE811"

/db_xref="taxon:4577"

/clone.lib="maize leaf DNA"

/note="PCR products amplified from genomic DNA"

BASE COUNT 67 a 107 c 83 g 71 t 2 others
ORIGIN

Query Match 100.0%; Score 12; DB 11; Length 330;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctgaggag 12
|||||
DB 80 GCCTCTGGGAG 91

Search completed: May 10, 2002, 16:15:54
Job time: 7024 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OH nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 68.34 Seconds
(without alignments)
43.131 Million cell updates/sec

Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 gctctcgggag 12

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/pdata/2/1na/5A.COMB.seq: *
2: /cgn2_6/pdata/2/1na/5B.COMB.seq: *
3: /cgn2_6/pdata/2/1na/6A.COMB.seq: *
4: /cgn2_6/pdata/2/1na/6B.COMB.seq: *
5: /cgn2_6/pdata/2/1na/PCTUS.COMB.seq: *
6: /cgn2_6/pdata/2/1na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 12 | 100.0 | 12 | US-09-243-335-1 | Sequence 1, Appl |
| 2 | 12 | 100.0 | 28 | US-09-243-335-41 | Sequence 41, Appl |
| 3 | 12 | 100.0 | 28 | US-09-243-335-46 | Sequence 46, Appl |
| 4 | 12 | 100.0 | 28 | US-09-243-335-47 | Sequence 47, Appl |
| 5 | 12 | 100.0 | 28 | US-09-243-335-48 | Sequence 48, Appl |
| 6 | 12 | 100.0 | 200 | US-09-243-335-3 | Sequence 3, Appl |
| 7 | 12 | 100.0 | 1279 | US-08-146-010A-4 | Sequence 4, Appl |
| 8 | 12 | 100.0 | 1279 | US-08-674-168-9 | Sequence 9, Appl |
| 9 | 12 | 100.0 | 1363 | US-08-776-088-21 | Sequence 21, Appl |
| 10 | 12 | 100.0 | 1363 | PCT-US95-09145A-21 | Sequence 21, Appl |
| 11 | 12 | 100.0 | 1875 | US-08-878-474-4 | Sequence 4, Appl |
| 12 | 12 | 100.0 | 1938 | US-08-278-635B-1 | Sequence 1, Appl |
| 13 | 12 | 100.0 | 1938 | US-08-464-258B-1 | Sequence 1, Appl |
| 14 | 12 | 100.0 | 1938 | US-08-471-961-1 | Sequence 1, Appl |
| 15 | 12 | 100.0 | 2374 | US-08-466-589-5 | Sequence 5, Appl |
| 16 | 12 | 100.0 | 2374 | US-08-700-636-5 | Sequence 5, Appl |
| 17 | 12 | 100.0 | 2374 | US-08-467-574-5 | Sequence 5, Appl |
| 18 | 12 | 100.0 | 2374 | US-09-217-345-5 | Sequence 5, Appl |
| 19 | 12 | 100.0 | 2540 | US-08-446-919A-1 | Sequence 1, Appl |
| 20 | 12 | 100.0 | 2577 | US-08-209-521-25 | Sequence 25, Appl |
| 21 | 12 | 100.0 | 2655 | US-08-456-200B-10 | Sequence 10, Appl |
| 22 | 12 | 100.0 | 4837 | US-09-629-616-1 | Sequence 1, Appl |
| 23 | 12 | 100.0 | 5176 | US-09-182-024A-1 | Sequence 1, Appl |
| 24 | 12 | 100.0 | 5434 | US-08-841-349-1 | Sequence 1, Appl |
| 25 | 12 | 100.0 | 7032 | US-08-149-097D-24 | Sequence 24, Appl |
| 26 | 12 | 100.0 | 7032 | US-08-949-386-24 | Sequence 24, Appl |
| 27 | 12 | 100.0 | 7032 | US-08-450-562-24 | Sequence 24, Appl |

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| c | 28 | 12 | 100.0 | 7032 | 4 | US-08-984-709A-24 | Sequence 24, Appl |
| c | 29 | 12 | 100.0 | 7089 | 3 | US-08-949-386-25 | Sequence 25, Appl |
| c | 30 | 12 | 100.0 | 7089 | 3 | US-08-450-562-25 | Sequence 25, Appl |
| c | 31 | 12 | 100.0 | 7089 | 4 | US-08-984-709A-25 | Sequence 25, Appl |
| c | 32 | 12 | 100.0 | 8310 | 3 | US-08-870-126-11 | Sequence 11, Appl |
| c | 33 | 12 | 100.0 | 14985 | 3 | US-08-652-972A-6 | Sequence 6, Appl |
| c | 34 | 12 | 100.0 | 14985 | 3 | PCT-US96-06231A-6 | Sequence 6, Appl |
| c | 35 | 11.6 | 96.7 | 130 | 3 | US-08-577-081A-7 | Sequence 7, Appl |
| c | 36 | 11 | 91.7 | 60 | 4 | US-08-406-030A-8 | Sequence 8, Appl |
| c | 37 | 11 | 91.7 | 60 | 4 | US-08-406-030A-9 | Sequence 9, Appl |
| c | 38 | 11 | 91.7 | 342 | 1 | US-08-235-83B-8 | Sequence 8, Appl |
| c | 39 | 11 | 91.7 | 342 | 2 | US-08-465-473B-8 | Sequence 8, Appl |
| c | 40 | 11 | 91.7 | 371 | 4 | US-08-961-810-36 | Sequence 36, Appl |
| c | 41 | 11 | 91.7 | 371 | 4 | US-08-352-902D-36 | Sequence 36, Appl |
| c | 42 | 11 | 91.7 | 502 | 4 | US-09-085-199B-39 | Sequence 39, Appl |
| c | 43 | 11 | 91.7 | 570 | 2 | US-08-633-682-1 | Sequence 1, Appl |
| c | 44 | 11 | 91.7 | 570 | 3 | US-08-936-772-1 | Sequence 1, Appl |
| c | 45 | 11 | 91.7 | 570 | 4 | US-09-395-918-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-243-335-1
; Sequence 1, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE.
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-243-335-1

Query Match 100.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctctcgggag 12
DB 1 gctctcgggag 12

RESULT 2
US-09-243-335-41
; Sequence 41, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; APPLICANT: Duzic, Edmit
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 28

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-41

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
Db 6 gcctctggggag 17

RESULT 3
US-09-243-335-46
Sequence 46, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-46

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
Db 6 gcctctggggag 17

RESULT 4
US-09-243-335-47
Sequence 47, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-47

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
Db 6 gcctctggggag 17

RESULT 5
US-09-243-335-48
Sequence 48, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-243-335-48

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
Db 6 gcctctggggag 17

RESULT 6
US-09-243-335-3
Sequence 3, Application US/09243335A
Patent No. 6197580
GENERAL INFORMATION:
APPLICANT: American Home Products Corp.
APPLICANT: Susulic, Vedrana S.
APPLICANT: Duzic, Edmir
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
FILE REFERENCE: 0630/0E791
CURRENT APPLICATION NUMBER: US/09/243.335A
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 200
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
US-09-243-335-3

Query Match 100.0%; Score 12; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
Db 61 gcctctggggag 72

RESULT 7

US-08-146-010A-4/C

; Sequence 4, Application US/08146010A

; Patent No. 5591577

; GENERAL INFORMATION:

; APPLICANT: TSUCHIYA, MAKOTO

; APPLICANT: MORIYA, MIKO

; APPLICANT: MIMA, KIYOSHI

; TITLE OF INVENTION: MOBILE GENETIC ELEMENT ORIGINATED FROM

; TITLE OF INVENTION: BREVIABACTERIUM STRAIN

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,010A

; FILING DATE: 12-NOV-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 52694/92

; FILING DATE: 11-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-649-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELETYPE: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1279 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Brevibacterium lactofermentum

; STRAIN: AJ2256

; FEATURE:

; NAME/KEY: insertion_seq

; LOCATION: 1..1279

; US-08-146-010A-4

; Query Match

; Best Local Similarity 100.0%; Score 12; DB 1; Length 1279;

; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 ggcctctggggag 12

; DB 136 gccctctggggag 125

; US-08-674-168-9/C

; Sequence 9, Application US/08674168

; Patent No. 5804414

; GENERAL INFORMATION:

; APPLICANT: MORIYA, MIKO

; APPLICANT: MATSUI, HIROSHI

; APPLICANT: YOKOZAKI, KENZO

; APPLICANT: HIRANO, SEIKO

; RESULT 8

; US-08-674-168-9/C

; Sequence 9, Application US/08674168

; Patent No. 5804414

; GENERAL INFORMATION:

; APPLICANT: MORIYA, MIKO

; APPLICANT: MATSUI, HIROSHI

; APPLICANT: YOKOZAKI, KENZO

; APPLICANT: HAYAKAWA, Atsushi

; APPLICANT: IZUT, Masako

; APPLICANT: SUGIMOTO, Masakazu

; TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING

; TITLE OF INVENTION: ARTIFICIAL TRANSPOSON

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; STREET: P.C.

; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/674,168

; FILING DATE: 01-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-166541

; FILING DATE: 30-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-810-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELETYPE: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1279 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Brevibacterium lactofermentum

; STRAIN: AJ12036

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: 1..14

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: 1266..1279

; US-08-674-168-9

; Query Match

; Best Local Similarity 100.0%; Score 12; DB 1; Length 1279;

; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 ggcctctggggag 12

; DB 136 gccctctggggag 125

; US-08-776-088-21/C

; Sequence 21, Application US/08776088

; Patent No. 5773579

; GENERAL INFORMATION:

; APPLICANT: Torczynski, Richard M.

; APPLICANT: Bollon, Arthur P.

; APPLICANT: Lung Cancer Marker

; NUMBER OF SEQUENCES: 22

; RESULT 9

; US-08-776-088-21/C

; Sequence 21, Application US/08776088

; Patent No. 5773579

; GENERAL INFORMATION:

; APPLICANT: Torczynski, Richard M.

; APPLICANT: Bollon, Arthur P.

; APPLICANT: Lung Cancer Marker

; NUMBER OF SEQUENCES: 22

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SIDLEY & AUSTIN
;; STREET: 1201 Elm Street, Suite 4500
;; CITY: Dallas
;; STATE: TX
;; COUNTRY: US
;; ZIP: 75270-2197
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/776,088
;; FILING DATE: 19-JUL-95
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eugenia S. Hansen
;; REGISTRATION NUMBER: 31,966
;; REFERENCE/DOCKET NUMBER: 10365/05011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 214-981-3300
;; TELEFAX: 214-981-3400
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1363 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-776-088-21

Query Match 100.0%; Score 12; DB 1; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
DB 183 gccctctggggag 172

RESULT 10
PCT-US95-09145A-21/C
; Sequence 21, Application PC/TUS9509145A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09145A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: John A. Harre
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35792CIPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 21:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1363 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; PCT-US95-09145A-21

Query Match 100.0%; Score 12; DB 5; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
DB 183 gccctctggggag 172

RESULT 11
US-08-878-474-4/C
; Sequence 4, Application US/08878474
; Patent No. 6133232
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumeester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,474
; FILING DATE: 18-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 60/020,150
; FILING DATE: 20-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 3100.002US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/248-5500
; TELEFAX: 415/362-5418
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-878-474-4

Query Match 100.0%; Score 12; DB 3; Length 1875;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcctcggggag 12
|||||
DB 769 gccctctggggag 758

RESULT 12
US-08-278-635B-1
Sequence 1, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-278-635B-1

Query Match 100.0%; Score 12; DB 1; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcggggag 12
|||||
DB 878 GCCTCTGGGAG 889

RESULT 13
US-08-464-258B-1
Sequence 1, Application US/08464258B
Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-464-258B-1

Query Match 100.0%; Score 12; DB 3; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccctcggggag 12
|||||
DB 878 GCCTCTGGGAG 889

RESULT 14
US-08-471-961-1
Sequence 1, Application US/08471961
Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1938 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: ALPHA 9
FEATURE:
NAME/KEY: CDS
LOCATION: 89..1525
US-08-471-961-1

Query Match 100.0%; Score 12; DB 3; Length 1938;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 878 GCCTCTGGGGAG 889

RESULT 15
US-08-466-589-5
Sequence 5, Application US/08466589
GENERAL INFORMATION:
PATENT NO. 5837489
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2374 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..2067
US-08-466-589-5

Query Match 100.0%; Score 12; DB 2; Length 2374;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcctcggggag 12
|||||
DB 2237 GCCTCTGGGGAG 2248

```

Search completed: May 10, 2002, 15:39:25
Job time: 4835 sec

PT compounds capable of regulating beta3-AR (adrenergic receptor)

expression, is composed of three regulatory segments -

XX
XX
PS Claim 2: Page 57; 88pp; English.

CC The present sequence represent the core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.

XX
XX
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
DB 1 gcctctggggag 12

RESULT 2
AAA87942
ID AAA87942 standard; DNA: 28 BP.
XX
AC AAA87942;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:41.
XX
XX
XX Human: beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
XX regulation; identification; trans-activating factor; drug screening;
XX gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
XX WO200044901-A1.
XX
XX PD 03-AUG-2000.
XX
XX 01-FEB-2000; 2000WO-US02632.
XX
XX 01-FEB-1999; 99US-0243335.
XX
XX (AMHP) AMERICAN HOME PROD CORP.
XX
XX Susulic VS, Duzic E;
XX
XX WPI: 2000-482973/42.
XX
XX
XX New isolated nucleic acid useful for screening assays to identify
XX compounds capable of regulating beta3-AR (adrenergic receptor)
XX expression, is composed of three regulatory segments -
XX
XX Example 1; Fig 7; 88pp; English.

CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.

XX
XX
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.

XX
XX
SQ Sequence 28 BP; 4 A; 10 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
|||||
DB 6 gcctctggggag 17

RESULT 3
AAA87947
ID AAA87947 standard; DNA: 28 BP.
XX
AC AAA87947;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:46.
XX
XX
XX Human: beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
XX regulation; identification; trans-activating factor; drug screening;
XX gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
XX WO200044901-A1.
XX
XX PN 03-AUG-2000.
XX
XX PD 01-FEB-2000; 2000WO-US02632.
XX
XX PF 01-FEB-1999; 99US-0243335.
XX
XX PR 01-FEB-1999; 99US-0243335.
XX
XX PA (AMHP) AMERICAN HOME PROD CORP.
XX
XX PI Susulic VS, Duzic E;
XX
XX WPI: 2000-482973/42.
XX
XX
XX New isolated nucleic acid useful for screening assays to identify
XX compounds capable of regulating beta3-AR (adrenergic receptor)
XX expression, is composed of three regulatory segments -
XX
XX Example 1; Fig 7; 88pp; English.

CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.

XX
XX
SQ Sequence 28 BP; 3 A; 10 C; 8 G; 7 T; 0 other;

| | | | | |
|--------------------------|---------|--------------------|--------|-------------------|
| Query Match | 100.0%; | Score 12; | DB 21; | Length 28; |
| Best Local Similarity | 100.0%; | Pred. No. 1.6e+03; | | |
| Matches 12; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

| Qy | 1 | gcctctgggag | 12 |
|----|---|-------------|----|
| Db | 6 | gcctctgggag | 17 |

| RESULT | 4 |
|----------|--------------------------------|
| AAA87948 | |
| ID | AAA87948 standard; DNA; 28 BP. |

| | |
|----|---------------------------|
| AC | AAA87948; |
| XX | |
| DT | 07-DEC-2000 (first entry) |

Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:47

Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter
regulation; identification; trans-activating factor; drug screening;
gene expression regulation; obesity; type II diabetes; mutation; ss.

| | |
|----|-----------------|
| OS | Homo sapiens. |
| XX | |
| PN | WO200044901-A1. |
| XY | |

PD 03-AUG-2000

PF 01-FEB-2000; 2000WO-US02632.
yy

PR 01-FEB-1999; 99US-0243335.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Susul1c VS, Duz1c E;

WPI: 2000-482973/42.

PT New Isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -

PS Example 1; Flg 7; 88pp; English.

CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.

Sequence 28 BP; 6 A; 9 C; 9 G; 4 T; 0 other;

| | | | | |
|-----------------------|-----------------|---------------|-----------|------------|
| Query Match | 100.0% | Score 12: | DB 21: | Length 28: |
| Best Local Similarity | 100.0% | Pred. No. | 1.6e+03: | |
| Matches 12: | Conservative 0: | Mismatches 0: | Indels 0: | Gaps 0 |

| Qy | 1 | gcctctgggag | 12 |
|----|---|-------------|----|
| | | | |
| Db | 6 | gcctctgggag | 17 |

| | |
|----------|--------------------------------|
| RESULT | 5 |
| AAA87949 | |
| ID | AAA87949 standard; DNA; 28 BP. |
| XY | |

AC AAA87949

DT 07-DEC-2000 (first entry)

Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:48.

KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter
 KW regulation; identification; trans-activating factor; drug screening;
 KW gene expression regulation; obesity; type II diabetes; mutation; ss.

| | |
|----|-----------------|
| OS | Homo sapiens. |
| XX | |
| PN | W0200044901-A1. |

03-AUG-2000 PD

PF 01-FEB-2000; 2000WO-US02632

PR 01-FEB-1999; 99US-0243335

PA (AMHP) AMERICAN HOME PROD CORP.

PI Susulic VS, Duzic E

DR WPI; 2000-482973/42.

PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -

PS Example 1; Fig 7; 88pp; English

CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.

Sequence 28 BP; 5 A; 7 C; 11 G; 5 T; 0 other.

| | | | | |
|--------------------------|--------|------------|----------|------------|
| Query Match | 100.0% | Score 12: | DB 21: | Length 28: |
| Best Local Similarity | 100.0% | Pred. NC: | 1.6e+03: | |
| Matches 12: Conservative | 0: | Mismatches | 0: | Indels 0: |
| | | | | Gaps 0 |

| Qy | 1 | gcctctgggag | 12 |
|----|---|-------------|----|
| Db | 6 | gcctctgggag | 17 |

RESULT 6
ABA76256
ID ABA76256 standard; DNA; 113 BP

| | |
|----|---------------------------|
| AC | ABA76256; |
| XX | |
| DT | 01-FEB-2002 (first entry) |

```

XX Human foetal liver single exon nucleic acid probe #24561.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW
XX Homo sapiens.
OS
XX WO200157277-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00669.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI: 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver.
XX
XX Claim 4: SEQ ID NO 24561; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
SQ

```

```

Query Match          100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

1 gcctctggggag 12
|||||
94 gcctctggggag 105

RESULT 7
ABA40796
ID ABA40796 standard; DNA; 113 BP.
XX
XX ABA40796;
AC
XX
XX 23-JAN-2002 (first entry)
DT
XX
XX Probe #19262 for gene expression analysis in human heart cell sample.
DE
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX
XX 09-AUG-2001.
PD

```

```

XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI: 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 4: SEQ ID NO 19262; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosis diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
SQ

```

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Query Match          100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

1 gcctctggggag 12
|||||
94 gcctctggggag 105

RESULT 8
AAK24907
ID AAK24907 standard; DNA; 113 BP.
XX
XX AAK24907;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human brain expressed single exon probe SEQ ID NO: 24898.
DE
XX
XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00667.
PE
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR

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| | | |
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| PR | 21-SEP-2000; | 2000US-0234687. |
| PR | 27-SEP-2000; | 2000US-0236359. |
| PR | 04-OCT-2000; | 2000GB-0024263. |
| XX | | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| XX | | |
| PI | Penn SG, Hanzel DK, Chen W, Rank DR; | |
| XX | | |
| DR | WPI: 2001-483446/52. | |
| XX | | |
| PT | Single exon nucleic acid probes for analyzing gene expression in human | |
| PT | brains - | |
| XX | | |
| PS | Example 4: SEQ ID NO: 24898; 650pp + Sequence Listing: English. | |
| XX | | |
| CC | The present invention provides a number of single exon nucleic acid | |
| CC | probes which are derived from genomic sequences expressed in the human | |
| CC | brain. They can be used to measure gene expression in brain cell samples, | |
| CC | which may enable the diagnosis and improved treatment of nervous system | |
| CC | diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, | |
| CC | epilepsy and cancers. The present sequence is one of the probes of the | |
| CC | invention. | |
| XX | | |
| SQ | Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other; | |
| XX | | |
| Query Match | 100.0%; Score 12; DB 22; Length 113; | |
| Best Local Similarity | 100.0%; Pred. No. 1.5e+03; | |
| Matches 12; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | |
| Oy | 1 ggcctctggggag 12 | |
| | | |
| Db | 94 ggcctctggggag 105 | |
| XX | | |
| RESULT 9 | | |
| AAK50902 | | |
| ID | AAK50902 standard; DNA: 113 BP. | |
| XX | | |
| AC | AAK50902; | |
| XX | | |
| DT | 06-NOV-2001 (first entry) | |
| XX | | |
| DE | Human bone marrow expressed single exon probe SEQ ID NO: 25459. | |
| XX | | |
| KW | Human; bone marrow expressed exon; gene expression analysis; probe; | |
| KM | microarray; cancer; leukemia; lymphoma; myeloma; ss. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200157276-A2. | |
| XX | | |
| PD | 09-AUG-2001. | |
| XX | | |
| PF | 30-JAN-2001; 2001WO-US00668. | |
| XX | | |
| PR | 04-FEB-2000; 2000US-0180312. | |
| PR | 26-MAY-2000; 2000US-0207456. | |
| PR | 30-JUN-2000; 2000US-0608408. | |
| PR | 03-AUG-2000; 2000US-0632366. | |
| PR | 21-SEP-2000; 2000US-0234687. | |
| PR | 27-SEP-2000; 2000US-0236359. | |
| PR | 04-OCT-2000; 2000GB-0024263. | |
| XX | | |
| PA | (MOLE-) MOLECULAR DYNAMICS INC. | |
| XX | | |
| PI | Penn SG, Hanzel DK, Chen W, Rank DR; | |
| XX | | |
| DR | WPI: 2001-488900/53. | |
| XX | | |
| PT | Human genome-derived single exon nucleic acid probes useful for | |
| PT | analyzing gene expression in human bone marrow - | |

XX Example 4; SEQ ID NO: 25459; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention.

XX
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 gccctctggggag 12
|||||
Db 94 gccctctggggag 105

RESULT 10
AA127940
ID AA127940 standard; DNA; 113 BP.
XX
XX AA127940;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #17873 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAR-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID NO 17873; 487bp; English.

CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||
 DB 94 gcctctggggag 105

RESULT 11

AAA87904
 ID AAA87904 standard; DNA; 200 BP.

AC AAA87904;

DT 07-DEC-2000 (first entry)

DE Human beta-3-adrenergic receptor 5' flanking region SEQ ID NO:3.

Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter; regulation; identification; trans-activating factor; drug screening; gene expression regulation; obesity; type II diabetes; ds.

OS Homo sapiens.

MO200044901-A1.

PD 03-AUG-2000.

PF 01-FEB-2000; 2000MO-US02632.

PR 01-FEB-1999; 99US-0243335.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Susulic VS, Duzic E;

WP1; 2000-482973/42.

New isolated nucleic acid useful for screening assays to identify compounds capable of regulating beta3-AR (adrenergic receptor) expression, is composed of three regulatory segments -

Claim 10; Fig 6A; 88pp; English.

The present invention describes a core nucleotide sequence from the B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory region. The core nucleotide sequence binds to a B-segment-binding trans-activating factor. Recombinant vectors under control of the transcription regulation region comprising nucleotide sequences containing the core nucleotide sequence from the B segment of the human beta-3-AR regulatory region provide a substrate for high throughput assays, particularly reporter gene assays to identify compounds capable of increasing or decreasing the level of expression of beta-3-AR. The nucleotide sequences can be used for regulating gene expression and for drug screening. It is envisaged that beta-3-AR stimulation may have beneficial effects in the treatment of obesity and type II diabetes. The present sequence represents the human beta-3-adrenergic receptor 5' flanking region, which is used in the exemplification of the present invention.

Sequence 200 BP; 25 A; 70 C; 37 G; 68 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||
 DB 61 gcctctggggag 72

RESULT 12

AAC15250/C
 ID AAC15250 standard; CDNA; 227 BP.

AC AAC15250;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 19325.

Human; 5' EST; expressed sequence tag; secreted protein; CDNA isolation; gene therapy; chromosome mapping; ss.

OS Homo sapiens.

EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

WP1; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

Claim 1; SEQ ID 19325; 71pp + CD-ROM; English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

Sequence 227 BP; 50 A; 53 C; 67 G; 53 T; 4 other;

Query Match 100.0%; Score 12; DB 21; Length 227;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
 |||
 DB 169 GCTCTGTGGGAG 158

RESULT 13

AAS30782
 ID AAS30782 standard; CDNA; 234 BP.

AC AAS30782;

DT 04-DEC-2001 (first entry)

DE Human cDNA encoding G protein-coupled receptor ngPCR-83.

XX Human: G protein-coupled receptor: ngPCR-x: ss: antiviral; analgesic;
KM cyclostatic; caritane; antidiabetic; anorectic; hypotensive; hypertensive;
KM antiparkinsonian; nootropic; neuroprotective; antidepressant;
KM viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
KM cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
KM obesity; anorexia; hypotension; hypertension; myocardial infarction;
KM atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
KM schizophrenia; migraine; major depression; anxiety; mental disorder;
KM manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
XX
OS Homo sapiens.
XX
PN W020016750-A2.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-US07322.
XX
PR 08-MAR-2000; 2000US-0187581.
PR 08-MAR-2000; 2000US-0187582.
PR 08-MAR-2000; 2000US-0187714.
PR 08-MAR-2000; 2000US-0187715.
PR 08-MAR-2000; 2000US-0187825.
PR 08-MAR-2000; 2000US-0187828.
PR 08-MAR-2000; 2000US-0187829.
PR 08-MAR-2000; 2000US-0187830.
PR 08-MAR-2000; 2000US-0187833.
PR 08-MAR-2000; 2000US-0187874.
PR 08-MAR-2000; 2000US-0187930.
PR 08-MAR-2000; 2000US-0188049.
PR 08-MAR-2000; 2000US-0189294.
PR 08-MAR-2000; 2000US-0189299.
PR 08-MAR-2000; 2000US-0189298.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogell G, Wood LS;
XX
DR WPI: 2001-536778/59.
XX
DR P-PSDB; AAU19213.
XX
PT Isolated nucleic acid molecules encoding G protein-coupled receptors
PT termed ngPCR-x, useful in the treatment and diagnosis of viral
PT infections, cancers and mental disorders (e.g. Parkinson's disease and
PT schizophrenia) -
XX
PS Claim 4; Page 201; 336pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules encoding
CC G protein-coupled receptors termed ngPCR-x. ngPCR-x polynucleotides,
CC polypeptides, and modulators may be used in the treatment of diseases and
CC conditions such as infections, such as viral infections caused by HIV-1
CC (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
CC cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
CC anorexia, hypotension, hypertension, myocardial infarction,
CC atherosclerosis), Parkinson's disease, and psychotic and
CC neurological disorders, including schizophrenia, migraine, major
CC depression, anxiety, mental disorder, manic depression, and
CC dyskinesias, such as Huntington's disease or Tourette's Syndrome.
CC and many other diseases and syndromes listed in the specification.
CC ngPCR-x polynucleotides and polypeptides, as well as ngPCR-x
CC modulators, may also be used in diagnostic assays for such diseases or
CC conditions. The present sequence encodes a G protein-coupled
CC receptor of the invention.
XX
SQ Sequence 234 BP; 56 A; 64 C; 65 G; 49 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
Db 100 gcctctggggag 111
RESULT 14
AAC48449
ID AAC48449 standard; DNA; 294 BP.
XX
AC AAC48449;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57523.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 02-JUL-1999; 99US-0142154.
 PR 06-JUL-1999; 99US-0142055.
 PR 08-JUL-1999; 99US-0142290.
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 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
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 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 12; DB 21; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcctctggggag 12
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 Ddb 209 gcctctggggag 220

RESULT 15
 ABAS1365/c

ID ABA51365 standard; DNA; 305 BP.
 XX
 AC ABA51365;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #10060.
 XX
 KW Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157271-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00662.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-496933/54.
 XX
 PA New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes
 XX
 PS Claim 4: SEQ ID NO 10060; 327bp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BR 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 305 BP; 90 A; 67 C; 110 G; 38 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gccctcgggag 12
 |||||
 DB 22 GCCTCTGGGAG 11

Mon May 13 08:57:59 2002

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